

What is claimed is:

1 1. A method for predicting single nucleotide polymorphisms, comprising the
2 steps of:

3 obtaining a variation predictiveness matrix; and

4 predicting one or more single nucleotide polymorphisms of a nucleic acid sequence
5 based on the variation predictiveness matrix.

1 2. The method of claim 1 further comprising one or more nucleic acid sequences
2 with chemical modifications.

1 3. The method of claim 2, wherein the chemical modifications include
2 methylation or other chemical groups that incorporate additional charge, polarizability,
3 hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid
4 bases or to the nucleic acid sequence as a whole.

1 4. The method of claim 1, wherein the step of predicting the likelihood of one or
2 more single nucleotide polymorphisms comprises the steps of:

3 comparing the nucleic acid sequence one or more bases at a time with the variation
4 predictiveness matrix to assign a variation value to bases in the nucleic acid sequence; and

5 selecting the polymorphisms that will likely cause a variation in one or more bases of
6 the nucleic sequence based on the variation value.

1 5. The method of claim 4, wherein the variation in one or more bases is
2 nonsynonymous.

1 6. The method of claim 4, wherein the variation in one or more bases is
2 synonymous.

1 7. The method of claim 1, further comprising the step of generating a dataset of
2 single nucleotide polymorphisms for one or more nucleic acid sequences.

1 8. The method of claim 1, wherein the step of obtaining a variation
2 predictiveness matrix, further comprises the steps of:

3 calculating a variation frequency from a first base to a second base in a dataset of two
4 or more genes; and

5 generating the variation predictiveness matrix from the calculated variation
6 frequency.

1 9. The method of claim 8 wherein the dataset comprises genes with nucleic acid
2 chemical modifications.

1 10. The method of claim 9, wherein the chemical modifications include
2 methylation or other chemical groups that incorporate additional charge, polarizability,
3 hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid
4 bases or to the nucleic acid as a whole.

1 11. The method of claim 8, wherein the variation frequency is determined from a
2 known mutation dataset.

1 12. The method of claim 8, wherein the variation frequency is determined from a
2 dataset of known diseases.

1 13. The method of claim 8, wherein the variation frequency is determined from a
2 dbSNP database.

1 14. The method of claim 8, wherein the variation frequency is determined from a
2 non-human mutation database.

1 15. The method of claim 8, wherein the variation frequency is determined from a
2 disease-specific database.

1 16. The method of claim 8, wherein the variation frequency is determined from a
2 non-human disease database.

1 17. The method of claim 8, wherein the variation frequency is determined from a
2 HGMD database.

1 18. The method of claim 8, wherein the variation frequency is determined from a
2 linkage database.

1 19. The method of claim 8, wherein the variation frequency is determined from a
2 splice variant database.

1 20. The method of claim 8, wherein the variation frequency is determined from a
2 translocation database.

1 21. The method of claim 8, wherein the variation frequency is determined from a
2 database of known mutations.

1 22. The method of claim 8, wherein the variation frequency is further adjusted for
2 wild type genes.

1 23. The method of claim 8, wherein the variation frequency is further adjusted for
2 engineered or non-naturally occurring genes.

1 24. The method of claim 8, wherein the variation frequency is further adjusted for
2 conservative polymorphisms.

1 25. The method of claim 8, wherein the variation frequency is further adjusted for
2 non-conservative polymorphisms.

1 26. The method of claim 8, wherein the variation frequency is further adjusted for
2 cDNA stability.

1 27. The method of claim 8, wherein the variation frequency is further adjusted for
2 predicted DNA structure.

1 28. The method of claim 8, wherein the variation frequency is further adjusted for
2 predicted RNA structure.

1 29. The method of claim 8, wherein the variation frequency is further adjusted for
2 predicted protein structure.

1 30. The method of claim 8, wherein the variation frequency is further adjusted for
2 post-translational modification sequences.

1 31. The method of claim 8, wherein the variation frequency is further adjusted for
2 protein stability.

1 32. The method of claim 8, wherein the variation frequency is further adjusted for
2 predicted protein transport.

1 33. The method of claim 8, wherein the variation frequency is further adjusted for
2 shuffled genes.

1 34. The method of claim 8, wherein the variation frequency is further adjusted for
2 site-directed mutagenesis genes.

1 35. The method of claim 8, wherein the variation frequency is further adjusted for
2 methylated sequences

1 36. The method of claim 8, wherein the variation frequency is further adjusted for
2 epigenetic variation.

1 37. The method of claim 8, wherein the nucleic acid sequence comprises a cDNA
2 sequence.

1 38. The method of claim 8, wherein the nucleic acid sequence comprises genomic
2 sequence.

1 39. The method of claim 8, wherein the nucleic acid sequence comprises an
2 intron/exon boundary.

1 40. The method of claim 8, wherein the nucleic acid sequence comprises a
2 transcriptional control sequence.

1 41. The method of claim 8, wherein the nucleic acid sequence comprises a
2 transport control sequence.

1 42. The method of claim 8, wherein the nucleic acid sequence comprises a
2 translational control sequence.

1 43. The method of claim 8, wherein the nucleic acid sequence comprises a
2 transcriptional control sequence.

1 44. The method of claim 8, wherein the nucleic acid sequence comprises a
2 splicing control sequence.

1 45. The method of claim 1, wherein the step of obtaining a variation
2 predictiveness matrix correlates the frequency of a first codon mutation to a second codon
3 mutation with a variation predictiveness value of a nucleic acid sequence from one to ten
4 bases at a time.

1 46. The method of claim 1, wherein in the variation predictiveness matrix is
2 normalized for the codon usage of a target organism.

1 47. The method of claim 1, wherein the variation predictiveness matrix is
2 generated from a mutant gene dataset that comprises all mutant genes in a mutant gene
3 database.

1 48. The method of claim 1, wherein the variation predictiveness matrix is
2 generated from a mutant gene dataset that comprises all mutant genes in a mutant gene
3 database minus the known mutant genes of the mutant gene dataset.

1 49. The method of claim 1, where the nucleic acid sequence comprises an entire
2 genome.

1 50. The method of claim 1, where the nucleic acid sequence comprises a human
2 genome.

1 51. The method of claim 1, where the nucleic acid sequence comprises a gene
2 cluster for a target human disease.

1 52. The method of claim 1, where the variation predictiveness matrix is based on
2 a mutant gene dataset that comprises a human mutation database.

1 53. The method of claim 1, wherein the steps are affected by a computer program.

1 54. The method of claim 53, wherein the computer program is SNIDE.

1 55. The method of claim 53, wherein the computer program is SNooP.

1 56. The method of claim 1, wherein the variation predictiveness matrix is
2 determined in silico from a human mutant database.

1 57. The method of claim 1, wherein the step of predicting a likelihood of one or
2 more single nucleotide polymorphisms is determined in silico.

1 58. A method for creating a variation predictiveness value for use in a variation
2 predictiveness matrix, comprising the steps of:

3 calculating the variation frequency from a first nucleic acid to a second nucleic acid
4 in a dataset of two or more variations; and

5 determining a variation predictiveness value from the calculated variation frequency.

1 59. The method of claim 58, further comprising the step of generating a variation
2 predictiveness matrix that correlates the frequency of a first to a second variation with the
3 variation predictiveness value.

1 60. The method of claim 58, wherein the dataset comprises genes with nucleic
2 acid chemical modifications.

1 61. The method of claim 60, wherein the chemical modifications include
2 methylation or other chemical groups that incorporate additional charge, polarizability,

3 hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid
4 bases or to the nucleic acid as a whole.

1 62. The method of claim 58, wherein the variation frequency is determined from a
2 known mutation dataset.

1 63. The method of claim 58, wherein the variation frequency is determined from a
2 dataset of known diseases.

1 64. The method of claim 58, wherein the variation frequency is determined from a
2 dbSNP database.

1 65. The method of claim 58, wherein the variation frequency is determined from a
2 non-human mutation database.

1 66. The method of claim 58, wherein the variation frequency is determined from a
2 disease-specific database.

1 67. The method of claim 58, wherein the variation frequency is determined from a
2 non-human disease database.

1 68. The method of claim 58, wherein the variation frequency is determined from a
2 HGMD database.

1 69. The method of claim 58, wherein the variation frequency is determined from a
2 linkage database.

1 70. The method of claim 58, wherein the variation frequency is determined from a
2 splice variant database.

1 71. The method of claim 58, wherein the variation frequency is determined from a
2 translocation database.

1 72. The method of claim 58, wherein the variation frequency is determined from a
2 database of known mutations.

1 73. The method of claim 58, wherein the variation frequency is further adjusted
2 for wild type genes.

1 74. The method of claim 58, wherein the variation frequency is further adjusted
2 for engineered or non-naturally occurring genes.

1 75. The method of claim 58, wherein the variation frequency is further adjusted
2 for conservative polymorphisms.

1 76. The method of claim 58, wherein the variation frequency is further adjusted
2 for non-conservative polymorphisms.

1 77. The method of claim 58, wherein the variation frequency is further adjusted
2 for cDNA stability.

1 78. The method of claim 58, wherein the variation frequency is further adjusted
2 for predicted DNA structure.

1 79. The method of claim 58, wherein the variation frequency is further adjusted
2 for predicted RNA structure.

1 80. The method of claim 58, wherein the variation frequency is further adjusted
2 for predicted protein structure.

1 81. The method of claim 58, wherein the variation frequency is further adjusted
2 for post-translational modification sequences.

1 82. The method of claim 58, wherein the variation frequency is further adjusted
2 for protein stability.

1 83. The method of claim 58, wherein the variation frequency is further adjusted
2 for predicted protein transport.

1 84. The method of claim 58, wherein the variation frequency is further adjusted
2 for shuffled genes.

1 85. The method of claim 58, wherein the variation frequency is further adjusted
2 for site-directed mutagenesis genes.

1 86. The method of claim 58, wherein the variation frequency is further adjusted
2 for methylated sequences

1 87. The method of claim 58, wherein the variation frequency is further adjusted
2 for epigenetic variation.

1 88. The method of claim 58, wherein the variations comprise a cDNA sequence.

1 89. The method of claim 58, wherein the variations comprise genomic sequence.

1 90. The method of claim 58, wherein variations comprise an intron/exon
2 boundary.

1 91. The method of claim 58, wherein variations comprise exons.

1 92. The method of claim 58, wherein variations comprise other SNPs.

1 93. The method of claim 58, wherein variations comprise inversions.

1 94. The method of claim 58, wherein variations comprise deletions.

1 95. The method of claim 58, wherein variations comprise splice variations.

1 96. The method of claim 58, wherein variations comprise translocations.

1 97. The method of claim 58, wherein variations comprise a transcriptional control
2 sequence.

1 98. The method of claim 58, wherein variations comprise a transport control
2 sequence.

1 99. The method of claim 58, wherein variations comprise a translational control
2 sequence.

1 100. The method of claim 58, wherein variations comprise a transcriptional control
2 sequence.

1 101. The method of claim 58, wherein variations comprise a splicing control
2 sequence.

1 102. The method of claim 59, wherein in the variation predictiveness matrix is
2 normalized for the nucleotide usage of a target organism.

1 103. The method of claim 59, wherein the variation predictiveness matrix is
2 generated from a mutant gene dataset that comprises all mutant genes in a mutant gene
3 database.

1 104. The method of claim 58, wherein the variation predictiveness matrix is
2 generated from a mutant gene dataset that comprises all mutant genes in a mutant gene
3 database minus the known mutant genes of the mutant gene dataset.

1 105. The method of claim 58, where the nucleic acid comprises one or more bases.

1 106. The method of claim 58, where the nucleic acid comprises DNA.

1 107. The method of claim 58, where the nucleic acid comprises RNA.

1 108. The method of claim 58, where the nucleic acid comprises a triplet.

1 109. The method of claim 58, The method of claim 16, where the nucleic acid
2 comprises a codon.

1 110. The method of claim 58, The method of claim 16, where the nucleic acid
2 comprises one or more non-sequence base modifications.

1 111. The method of claim 58, where the nucleic acid comprises modified nucleic
2 acids.

1 112. The method of claim 58, wherein modified nucleic acids include methylation
2 or other chemical groups that incorporate additional charge, polarizability, hydrogen

3 bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to
4 the nucleic acid as a whole.

1 113. The method of claim 58, where the nucleic acid comprises an entire genome.

1 114. The method of claim 58, where the nucleic acid comprises a human genome.

1 115. The method of claim 58, where the nucleic acid comprises a gene cluster for a
2 target human disease.

1 116. The method of claim 58, where the variation predictiveness matrix is based on
2 a mutant gene dataset that comprises a human mutation database.

1 117. The method of claim 58, wherein the steps are affected by a computer
2 program.

1 118. The method of claim 58, wherein the computer program is SNIDE.

1 119. The method of claim 58, wherein the computer program is SNooP.

1 120. The method of claim 58, wherein the variation predictiveness value is
2 determined in silico from a human mutant database.

1 121. The method of claim 58, wherein the step of predicting a likelihood of one or
2 more single nucleotide variation is determined in silico.

1 122. A method for creating a polymorphism predictiveness value for use in a
2 mutation predictiveness matrix, comprising the steps of:

3 calculating the mutation frequency from a first codon to a second codon in a dataset
4 of two or more mutant genes; and

5 determining a polymorphism predictiveness value from the calculated mutation
6 frequency.

1 123. The method of claim 122, further comprising the step of generating a codon
2 polymorphism predictiveness matrix that correlates the frequency of a first to a second codon
3 mutation with the polymorphism predictiveness value.

1 124 The method of claim 122, wherein the dataset comprises nucleic acids with
2 chemical modifications.

1 125 The method of claim 124, wherein the chemical modifications include
2 methylation or other chemical groups that incorporate additional charge, polarizability,
3 hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid
4 bases or to the nucleic acid as a whole.

1 126 The method of claim 122, wherein the mutation frequency is determined from
2 a known mutation dataset.

1 127 The method of claim 122, wherein the mutation frequency is determined from
2 a dataset of known diseases.

1 128 The method of claim 122, wherein the mutation frequency is determined from
2 a dbSNP database.

1 129 The method of claim 122, wherein the mutation frequency is determined from
2 a non-human mutation database.

1 130 The method of claim 122, wherein the mutation frequency is determined from
2 a disease-specific database.

1 131 The method of claim 122, wherein the mutation frequency is determined from
2 a non-human disease database.

1 132. The method of claim 122, wherein the mutation frequency is determined from
2 a HGMD database.

1 133. The method of claim 122, wherein the mutation frequency is determined from
2 a linkage database.

1 134. The method of claim 122, wherein the mutation frequency is determined from
2 a splice variant database.

1 135. The method of claim 122, wherein the mutation frequency is determined from
2 a translocation database.

1 136. The method of claim 122, wherein the mutation frequency is determined from
2 a database of known mutations.

1 137. The method of claim 122, wherein the mutation frequency is further adjusted
2 for wild type genes.

1 138. The method of claim 122, wherein the mutation frequency is further adjusted
2 for engineered or non-naturally occurring genes.

1 139. The method of claim 122, wherein the mutation frequency is further adjusted
2 for conservative polymorphisms.

1 140. The method of claim 122, wherein the mutation frequency is further adjusted
2 for non-conservative polymorphisms.

1 141. The method of claim 122, wherein the mutation frequency is further adjusted
2 for cDNA stability.

1 142. The method of claim 122, wherein the mutation frequency is further adjusted
2 for predicted DNA structure.

1 143. The method of claim 122, wherein the mutation frequency is further adjusted
2 for predicted RNA structure.

1 144. The method of claim 122, wherein the mutation frequency is further adjusted
2 for predicted protein structure.

1 145. The method of claim 122, wherein the mutation frequency is further adjusted
2 for post-translational modification sequences.

1 146. The method of claim 122, wherein the mutation frequency is further adjusted
2 for protein stability.

1 147. The method of claim 122, wherein the mutation frequency is further adjusted
2 for predicted protein transport.

1 148. The method of claim 122, wherein the mutation frequency is further adjusted
2 for shuffled genes.

1 149. The method of claim 122, wherein the mutation frequency is further adjusted
2 for site-directed mutagenesis genes.

1 150. The method of claim 122, wherein the mutation frequency is further adjusted
2 for methylated sequences

1 151. The method of claim 122, wherein the mutation frequency is further adjusted
2 for epigenetic variation.

1 152. The method of claim 122, wherein the mutant genes comprise a cDNA
2 sequence.

1 153. The method of claim 122, wherein the mutant genes comprise genomic
2 sequence.

1 154. The method of claim 122, wherein mutant genes comprise an intron/exon
2 boundary.

1 155. The method of claim 122, wherein mutant genes comprise exons.

1 156. The method of claim 122, wherein mutant genes comprise other SNPs.

1 157. The method of claim 122, wherein mutant genes comprise inversions.

1 158. The method of claim 122, wherein mutant genes comprise deletions.

1 159. The method of claim 122, wherein mutant genes comprise splice variations.

1 160. The method of claim 122, wherein mutant genes comprise translocations.

1 161. The method of claim 122, wherein mutant genes comprise a transcriptional
2 control sequence.

1 162. The method of claim 122, wherein mutant genes comprise a transport control
2 sequence.

1 163. The method of claim 122, wherein mutant genes comprise a translational
2 control sequence.

1 164. The method of claim 122, wherein mutant genes comprise a transcriptional
2 control sequence.

1 165. The method of claim 122, wherein mutant genes comprise a splicing control
2 sequence.

1 166. The method of claim 123, wherein in the codon polymorphism predictiveness
2 matrix is normalized for the codon usage of a target organism.

1 167. The method of claim 123, wherein the codon polymorphism predictiveness
2 matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant
3 gene database.

1 168. The method of claim 123, wherein the codon polymorphism predictiveness
2 matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant
3 gene database minus the known mutant genes of the mutant gene dataset.

1 169. The method of claim 122, where the codon comprises one or more bases.

1 170. The method of claim 122, where the codon comprises DNA.

1 171. The method of claim 122, where the codon comprises RNA.

1 172. The method of claim 122, where the codon comprises a triplet.

1 173. The method of claim 122, where the codon comprises a codon.

1 174. The method of claim 122, where the codon comprises one or more non-
2 sequence base modifications.

1 175. The method of claim 122, wherein the codon further comprises modifications.

1 176. The method of claim 122, wherein modifications include methylation or other
2 chemical groups that incorporate additional charge, polarizability, hydrogen bonding,
3 electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic
4 acid as a whole.

1 177. The method of claim 122, where the codon comprises an entire genome.

1 178. The method of claim 122, where the codon comprises a human genome.

1 179. The method of claim 122, where the codon comprises a gene cluster for a
2 target human disease.

1 180. The method of claim 122, where the codon polymorphism predictiveness
2 matrix is based on a mutant gene dataset that comprises a human mutation database.

1 181. The method of claim 122, wherein the step of predicting a likelihood of one or
2 more single nucleotide polymorphisms is determined in silico.

1 182. A method for creating a variation predictiveness matrix, comprising the steps
2 of:

3 calculating the variation frequency from a first nucleic acid to a second nucleic acid
4 in a dataset of two or more variations;

5 determining a variation predictiveness value from the calculated variation frequency;
6 and

7 generating a variation predictiveness matrix that correlates the frequency of a first to
8 a second nucleic acid with the variation predictiveness value.

1 183. The method of claim 182, wherein the dataset comprises nucleic acids with
2 chemical modifications.

1 184. The method of claim 183, wherein the chemical modifications include
2 methylation or other chemical groups that incorporate additional charge, polarizability,
3 hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid
4 bases or to the nucleic acid as a whole.

1 185. The method of claim 182, wherein the variation frequency is determined from
2 a variation dataset.

1 186. A method for creating a polymorphism predictiveness matrix, comprising the
2 steps of:

3 calculating the mutation frequency from a first codon to a second codon in a dataset
4 of two or more mutant genes;

5 determining a polymorphism predictiveness value from the calculated mutation
6 frequency; and

7 generating a codon polymorphism predictiveness matrix that correlates the frequency
8 of a first to a second codon mutation with the polymorphism predictiveness value.

1 187. The method of claim 186, wherein the dataset comprises nucleic acids with
2 chemical modifications.

1 188. The method of claim 187, wherein the chemical modifications include
2 methylation or other chemical groups that incorporate additional charge, polarizability,
3 hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid
4 bases or to the nucleic acid as a whole.

1 189. The method of claim 186, wherein in the codon polymorphism predictiveness
2 matrix is normalized for the codon usage of a target organism.

1 190. The method of claim 186, wherein the codon polymorphism predictiveness
2 matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant
3 gene database.

1 191. The method of claim 186, wherein the codon polymorphism predictiveness
2 matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant
3 gene database minus the known mutant genes of the mutant gene dataset.

1 192. The method of claim 186, wherein the codon comprises one or more bases.

1 193. The method of claim 186, where the codon comprises a triplet.

1 194. The method of claim 186, where the codon comprises a codon.

1 195. The method of claim 186, where the codon comprises one or more non-
2 sequence base modifications.

1 196. An isolated and purified nucleic acid comprising a predicted single nucleotide
2 variation of a nucleic acid sequence based on the variation predictiveness matrix sequence of
3 claim 1.

1 197. An isolated and purified nucleic acid comprising a predicted single nucleotide
2 polymorphism of a wild-type gene sequence based on the codon mutation predictiveness
3 matrix sequence of claim 1.

1 198. An apparatus for detecting a single nucleotide polymorphism comprising:

2 a substrate; and

3 one or more isolated and purified nucleic acids comprising a predicted single
4 nucleotide variation of a nucleic acid sequence based on a variation predictiveness matrix
5 sequence affixed to the substrate.

1 199. The apparatus of claim 198, wherein the substrate comprises a
2 microfabricated solid surface to which molecules may be attached through either covalent or
3 non-covalent bonds.

1 200. The apparatus of claim 198, wherein the substrate further comprises
2 Langmuir-Bodgett films, glass, functionalized glass, germanium, silicon, PTFE, polystyrene,
3 gallium arsenide, gold, silver, or any materials comprising amino, carboxyl, thiol or hydroxyl
4 functional groups incorporated on a planar or spherical surface.

1 201. An apparatus for detecting a single nucleotide polymorphism comprising:
2 a substrate; and

3 one or more isolated and purified nucleic acids comprising a predicted single
4 nucleotide polymorphism of a wild-type gene sequence based on a codon polymorphism
5 predictiveness matrix. sequence affixed to the substrate.

1 202. The apparatus of claim 201, wherein the substrate comprises a
2 microfabricated solid surface to which molecules may be attached through either covalent or
3 non-covalent bonds.

1 203. A computer program embodied on a computer readable medium for predicting
2 variations, comprising:

3 a code segment for creating variation predictiveness matrix from a nucleic acid
4 dataset;

5 a code segment for comparing a wild-type gene sequence with the variation
6 predictiveness matrix; and

7 a code segment for predicting variations in the wild-type gene sequence based on the
8 comparison.

1 204. A computer program embodied on a computer readable medium for predicting
2 polymorphisms, comprising:

3 a code segment for creating a codon mutation predictiveness matrix from a mutant
4 gene dataset;

5 a code segment for comparing a wild-type gene sequence with the codon
6 polymorphism predictiveness matrix; and

7 a code segment for predicting polymorphisms in the wild-type gene sequence based
8 on the comparison.

1 205. A polymorphism prediction dataset, comprising:

2 a first nucleic acid;

3 a second nucleic acid variation that correlates to a polymorphism from the first
4 nucleic acid; and

5 a variation predictiveness value determined from known variations in a variation
6 database for a target organism.

1 206. A polymorphism prediction dataset, comprising:

2 a first codon;

3 a second codon mutation that correlates to a mutation from the first codon; and

4 a codon polymorphism predictiveness value determined from known mutations in a
5 mutation database for a target organism.

1 207. A single nucleotide polymorphism determined by the method of claim 1.

1 208. A method for predicting single nucleotide polymorphisms, comprising the
2 steps of:

3 inputting each codon in a queried nucleic acid sequence;

4 determining each possible nonsynonymous mutation;

5 assigning a predictiveness value to that mutation based on the identity of the wild-
6 type and resultant codon; and

7 ranking of all predictiveness values to highlight the likely to occur and impact gene
8 function.

1 209. The method of claim 208, further comprising the steps of:
2 parsing one or more nucleic acid sequence input files having sequence information;
3 calculating an expected mutation liklihood according to a user-defined threshold; and
4 ranking of point mutation predictions by a ζ -value.

1 210. The method of claim 208, further comprising the step of generating a
2 delimited file suitable for a standard spreadsheet application.

1 211. An isolated and purified nucleic acid comprising SEQ ID NOS.: 1-12.

1 212. An isolated and purified nucleic acid comprising a cardiomyopathy disease
2 related SNP selected from the group consisting essentially of BDKRB2, EDNRA, ADRB1,
3 ADRB2, CREB1 and MCIP.

1 213. An isolated and purified nucleic acid of claim 211, wherein the SNP is Thr-
2 >Met substitution in BDKRB2 at position 383.